



SEQUENCE LISTING

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Neose Technologies, Inc.
Governors of the University of Alberta

<120> H. Pylori Fucosyltransferases

<130> 019957-019400US

<140> US 10/764,212

<141> 2004-01-22

<160> 81

<170> PatentIn Ver. 2.1

<210> 1

<211> 1461

<212> DNA

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1182 FutB fucosyltransferase
(1182B)

<400> 1

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<211> 486

<212> PRT

<213> Helicobacter pylori

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<223> H. pylori strain 1182 FutB fucosyltransferase

<400> 2

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 Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Asp Asn Pro Phe Ile Phe
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 Tyr Arg Asp Leu Asn Glu Pro Leu Ile Ser Ile Asp Asp Asp Leu Arg
 355 360 365
 Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn
 370 375 380
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 385 390 395 400
 Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu
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 Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val
 420 425 430
 Asn Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala
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 Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys Ile Tyr Arg
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<210> 3

<211> 1299

<212> DNA

<213> *Helicobacter pylori*

<220>

<223> *H. pylori* strain 1111 FutA fucosyltransferase
(1111FutA)

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 aacctgata aacctgcgga catcgctctt ggtaaccccc ttggatcagc cagaaaaatc 240
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 aacctctttg attacgccat aggctttgat gaattggact ttagagatcg ttatttgaga 360
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<212> PRT

<213> Helicobacter pylori

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<223> H. pylori strain 1111 FutA fucosyltransferase

<400> 4

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           20           25           30

Trp Gly Asp Glu Glu Ile Lys Lys Phe Lys Lys Ser Val Leu Tyr Phe
           35           40           45

Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Arg Asn Pro Asp Lys
           50           55           60

Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg Lys Ile
           65           70           75           80

Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu
           85           90           95

Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu
          100          105          110

Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala Tyr Leu
          115          120          125

His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu
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Gln Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys
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Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro
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Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro
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Arg Arg Asn Ala Phe Tyr Glu Ala Leu Asn Ala Ile Glu Pro Val Ala
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Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Val Lys Asn Lys
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 275 280 285
 Ala Ile Asp Tyr Ile Arg Tyr Leu His Thr His Pro Asn Ala Tyr Leu
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 Phe Tyr Gln Asn Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys Thr
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 340 345 350
 Arg Asp Leu Asn Glu Pro Ser Val Ser Ile Asp Gly Leu Arg Val Asn
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 Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp
 370 375 380
 Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala Ser Pro Leu
 385 390 395 400
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<210> 5

<211> 1458

<212> DNA

<213> *Helicobacter pylori*

<220>

<223> *H. pylori* strain 1218 FutB fucosyltransferase
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<400> 6

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Trp Trp Gly Asp Glu Glu Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr
    35              40              45

Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn
    50              55              60

Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys
    65              70              75              80

Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn
      85              90              95

Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
    100              105              110

Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg
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Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys
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Leu Lys Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe
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Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp
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Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala
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 Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr
 370 375 380
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 Val Asn Tyr Asp Asp Leu Arg Val Asn Cys Asp Asp Leu Arg Val Asn
 420 425 430
 Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala Ser
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 Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys Ile Tyr Arg Lys
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<220>
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 His Phe Ile Leu Ser Gln His Tyr Thr Ile Ala Leu His Arg Asn Pro
 50 55 60
 Asp Lys Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg
 65 70 75 80
 Lys Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu
 85 90 95
 Asn Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp
 100 105 110
 Glu Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp
 115 120 125
 Arg Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ala Pro Tyr
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Lys Ile Lys Ser Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His
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 165 170 175
 Asp Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn
 180 185 190
 Ala Pro Ile Arg Asn Ala Phe Tyr Glu Ala Leu Asn Ser Ile Glu Pro
 195 200 205
 Val Thr Gly Gly Gly Ser Val Arg Asn Thr Leu Gly Tyr Asn Val Lys
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 <212> DNA
 <213> Helicobacter pylori

<220>
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 (26695A.cod)

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 attcctattt attgggggag tcccagcgtg gcgaaagatt ttaaccctaa aagttttgtg 840
 aatgtgcatg atttcaacaa ctttgatgaa gcgattgatt atatcaaata cctgcacacg 900
 cacccaaacg cttattttaga catgctctat gaaaaccctt taaacaccct tgatgggaaa 960
 gttacttttt accaagattt gagtttttaa aaaatcctag atttttttaa aacgatttta 1020
 gaaaacgata cgattttatca caaatttctca acatctttca tgtgggagta cgatctgcat 1080
 aagccggttag tatccattga tgatttgagg gttaattatg atgatttgag gggttaattat 1140
 gaccggcttt tacaaaacgc ttcgccttta ttagaactct ctcaaaacac cactttttaa 1200
 atctatcgca aagcttatca aaaatccttg ctttggttgc gcgcggtgag aaagtgggtt 1260
 aaaaaattgg gtttgtaa 1278

<210> 12
 <211> 425
 <212> PRT
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 26695 FutA fucosyltransferase

<400> 12
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 1 5 10 15
 Lys Met Ala Ser Lys Ser Pro Pro Pro Pro Leu Lys Ile Ala Val Ala
 20 25 30

Asn Trp Trp Gly Asp Glu Glu Ile Lys Glu Phe Lys Lys Ser Val Leu
 35 40 45
 Tyr Phe Ile Leu Ser Gln Arg Tyr Ala Ile Thr Leu His Gln Asn Pro
 50 55 60
 Asn Glu Phe Ser Asp Leu Val Phe Ser Asn Pro Leu Gly Ala Ala Arg
 65 70 75 80
 Lys Ile Leu Ser Tyr Gln Asn Thr Lys Arg Val Phe Tyr Thr Gly Glu
 85 90 95
 Asn Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp
 100 105 110
 Glu Leu Asp Phe Asn Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala
 115 120 125
 His Leu His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ala Pro Tyr
 130 135 140
 Lys Leu Lys Asp Asn Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His
 145 150 155 160
 Phe Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asp Glu Ser
 165 170 175
 Asp Leu Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Ala Asn
 180 185 190
 Ala Pro Met Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro
 195 200 205
 Val Thr Gly Gly Gly Ser Val Arg Asn Thr Leu Gly Tyr Lys Val Gly
 210 215 220
 Asn Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu
 225 230 235 240
 Asn Ser Gln Gly Tyr Gly Tyr Val Thr Glu Lys Ile Leu Asp Ala Tyr
 245 250 255
 Phe Ser His Thr Ile Pro Ile Tyr Trp Gly Ser Pro Ser Val Ala Lys
 260 265 270
 Asp Phe Asn Pro Lys Ser Phe Val Asn Val His Asp Phe Asn Asn Phe
 275 280 285
 Asp Glu Ala Ile Asp Tyr Ile Lys Tyr Leu His Thr His Pro Asn Ala
 290 295 300
 Tyr Leu Asp Met Leu Tyr Glu Asn Pro Leu Asn Thr Leu Asp Gly Lys
 305 310 315 320
 Ala Tyr Phe Tyr Gln Asp Leu Ser Phe Lys Lys Ile Leu Asp Phe Phe
 325 330 335
 Lys Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Lys Phe Ser Thr Ser
 340 345 350

Phe Met Trp Glu Tyr Asp Leu His Lys Pro Leu Val Ser Ile Asp Asp
 355 360 365
 Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Arg Leu Leu
 370 375 380
 Gln Asn Ala Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys
 385 390 395 400
 Ile Tyr Arg Lys Ala Tyr Gln Lys Ser Leu Pro Leu Leu Arg Ala Val
 405 410 415
 Arg Lys Leu Val Lys Lys Leu Gly Leu
 420 425

<210> 13
 <211> 45 -
 <212> DNA
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 19C2 fucosyltransferase
 (19C2FutA.cod)

<400> 13
 atgttccaac ccttactaga cgcctttata gaaagtgctc caatt

45

<210> 14
 <211> 15
 <212> PRT
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 19C2 fucosyltransferase
 (19C2A.pep)

<400> 14
 Met Phe Gln Pro Leu Leu Asp Ala Phe Ile Glu Ser Ala Pro Ile
 1 5 10 15

<210> 15
 <211> 1973
 <212> DNA
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 1111 FutB fucosyltransferase

<400> 15
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 cattctaaag gcgaaatgct cctcgctttg caacgctcgt tgaatatcag taaagatcgc 180
 acttttagtcg tgggcgatgg ggcgaatgat ttgagcatgt tcaaacatgc ccatattaaa 240
 atcgctttta acgctaaaga ggttttataa cagcacgcca cgcattgcat caatgagcct 300
 aatctagccc taatcaagcc tttgatttac aaaaattttt tttgtaaaat tccctttaaa 360
 aggatagcca tgttccaacc cctattagac gcttatgtag aaagcgcttc cattgaaaaa 420
 atggcctcta aatctcccc cccctataaa atcgctgtgg cgaattggtg gggagatgaa 480
 gaaattaaag aatttaaaaa gagcgttctt tattttatct ttagccaacg ctacacaatc 540

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gccctccacc aaaaccccaa tgaattttca gatctagtct ttagcaatcc tcttggatca 600
gctagaaaaa tcttatcgta tcaaaacgct aaaagagtgt tttacaccgg tgaaaatgaa 660
gtccctaact tcaacctctt tgattacgcc ataggctttg atgaattgga ttttagagat 720
cgttatttga ggatgccttt atattatgat aggctacacc ataaagccga gagcgtgaat 780
gacaccactt cgcctacaa actcaaagac aacagccttt atactttaa aaaacccctc 840
catcaattta aagaaaacca ccctaattta gcgcagtcgt gaatgatgag agcgatcctt 900
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gaattatccc aaaacacctc ttttaaaatc tatcgcaaag cctatcaaag cctatcaaaa 1680
atccttacc cttattgcgc ccataaggag atgggttaaa aagtaagggtg tcttttaaga 1740
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gatgcgcca aaggattctt ctttagaaa gtttaaaagg cgtttgggca aaatctcgcc 1920
aaatacgata atgacttttg aagcgctgtt gtctaattgc caggctcgaa ttc 1973

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<210> 16

<211> 446

<212> PRT

<213> *Helicobacter pylori*

<220>

<223> *H. pylori* strain 1111 FutB fucosyltransferase

<400> 16

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Lys Met Ala Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala Asn
      20              25              30

Trp Trp Gly Asp Glu Glu Ile Lys Glu Phe Lys Lys Ser Val Leu Tyr
      35              40              45

Phe Ile Phe Ser Gln Arg Tyr Thr Ile Ala Leu His Gln Asn Pro Asn
      50              55              60

Glu Phe Ser Asp Leu Val Phe Ser Asn Pro Leu Gly Ser Ala Arg Lys
      65              70              75              80

Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn
      85              90              95

Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
      100             105             110

Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg
      115             120             125

Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys
      130             135             140

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Leu Lys Asp Asn Ser Leu Tyr Thr Leu Lys Lys Pro Ser His Gln Phe
 145 150 155 160
 Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asp Glu Ser Asp
 165 170 175
 Pro Leu Lys Arg Gly Val Val Ser Phe Val Ala Ser Asn Ala Asn Ala
 180 185 190
 Pro Met Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro Val
 195 200 205
 Thr Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Val Lys Asn
 210 215 220
 Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn
 225 230 235 240
 Ser Gln Gly Tyr Gly Tyr Val Thr Glu Lys Ile Leu Asp Ala Tyr Phe
 245 250 255
 Ser His Thr Ile Pro Ile Tyr Trp Gly Ser Pro Ser Val Ala Lys Asp
 260 265 270
 Phe Asn Pro Lys Glu Phe Val Asn Val His Asp Phe Asn Asn Phe Asp
 275 280 285
 Glu Ala Ile Asp Tyr Ile Lys Tyr Leu His Thr His Pro Asn Ala Tyr
 290 295 300
 Leu Asp Met Leu Tyr Glu Asn Pro Leu Asn Ala Leu Asp Gly Lys Ala
 305 310 315 320
 Tyr Phe Tyr Gln Asp Leu Ser Phe Lys Lys Ile Leu Ala Phe Phe Lys
 325 330 335
 Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Lys Ser Ser Thr Ser Phe
 340 345 350
 Met Trp Glu Cys Asp Leu Asp Glu Pro Leu Ala Ser Ile Asp Asp Leu
 355 360 365
 Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val
 370 375 380
 Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr
 385 390 395 400
 Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu Gln Asn Ala Ser Pro
 405 410 415
 Leu Leu Glu Leu Ser Gln Asn Thr Ser Phe Lys Ile Tyr Arg Lys Ala
 420 425 430
 Tyr Gln Lys Pro Ile Lys Asn Pro Tyr Pro Tyr Cys Ala Pro
 435 440 445

<210> 17
 <211> 1861
 <212> DNA
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 802 FutA fucosyltransferase

<400> 17
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 ttatttcaaa cgccatttga gtttgcctaa attggtttaa aggatagcca tgttccagcc 180
 cttactagac gcctttatag aaagtgcctc aattaaaaaa atgcctctga gttaccccc 240
 cctaaaaatc gctgtggcga attggtgggg aggcgctgaa gaatttaaaa agagcgctat 300
 gtatttcata ctaagccaac gctacacaat caccctccac caaaacccca acgaaccctc 360
 cgatctcgtc tttggcagtc ctattggagc agccagaaaa atcctatcct accaaaacac 420
 taaaagagtg ttttacgccg gtgaaaatga agtcctaata ttcaacctct ttgattacgc 480
 cataggcttt-gatgaattgg atttttagaga tcggtatttg agaatgcctt tatattatga 540
 tagactacac cataaagccg agagcgtgaa tgacaccacc gcgccttaca agattaaacc 600
 tgacagcctt tatacttttaa aaaaaccctc ccatacattt aaagaaaaaac acccccattt 660
 atgcgcagta gtgaatgatg agagcgatcc tttgaaaaga gggtttgcca gttttgtcgc 720
 aagcaaccct aacgctccta aaaggaacgc cttctatgac gctttaaatt ctattgagcc 780
 agttactggg ggagggagcg tgaaaaacac tttaggctat aaagttggaa acaaaaacga 840
 gtttttaagc caatacaaat tcaatctgtg ttttgaaaac tctcaaggct atggctatgt 900
 aaccgaaaaa atcattgacg cttacttttag ccataccatt cctattttatt gggggagtcc 960
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 cttacctttg ttgcgtgcca taaggagatg gggttaaaaaa ttgggtttgt aaaattgggg 1500
 gtaatcaaac cccttgcgct atcatcgag acgccacttt tctaaaacca gcgatattag 1560
 cccctaaaac aaaattagta gggctcttaa actcttttagc ggtttgagag acatttttat 1620
 aaatctcttt catgatgtgg tgtaatttcg catccaccac ttcaaaaactc caaggggtgca 1680
 tgctcgcggt ttgcgccatt tccaagccgc tcacgctcac cccccagca ttagccgcct 1740
 tgccataacc ataagaaatc ttagcctgta aaaacaattc aatcgcttca ttgcttgagg 1800
 gcatgttcgc cccttcagcc acgcatttgc acccattaga aaggagggtt ttgcggaatt 1860
 c 1861

<210> 18
 <211> 440
 <212> PRT
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 802 FutA fucosyltransferase

<400> 18
 Met Phe Gln Pro Leu Leu Asp Ala Phe Ile Glu Ser Ala Ser Ile Lys
 1 5 10 15
 Lys Met Pro Leu Ser Tyr Pro Pro Leu Lys Ile Ala Val Ala Asn Trp
 20 25 30
 Trp Gly Gly Ala Glu Glu Phe Lys Lys Ser Ala Met Tyr Phe Ile Leu
 35 40 45

Ser	Gln	Arg	Tyr	Thr	Ile	Thr	Leu	His	Gln	Asn	Pro	Asn	Glu	Pro	Ser	50	55	60
Asp	Leu	Val	Phe	Gly	Ser	Pro	Ile	Gly	Ala	Ala	Arg	Lys	Ile	Leu	Ser	65	70	75
Tyr	Gln	Asn	Thr	Lys	Arg	Val	Phe	Tyr	Ala	Gly	Glu	Asn	Glu	Val	Pro	85	90	95
Asn	Phe	Asn	Leu	Phe	Asp	Tyr	Ala	Ile	Gly	Phe	Asp	Glu	Leu	Asp	Leu	100	105	110
Arg	Asp	Arg	Tyr	Leu	Arg	Met	Pro	Leu	Tyr	Tyr	Asp	Arg	Leu	His	His	115	120	125
Lys	Ala	Glu	Ser	Val	Asn	Asp	Thr	Thr	Ala	Pro	Tyr	Lys	Ile	Lys	Pro	130	135	140
Asp	Ser	Leu	Tyr	Thr	Leu	Lys	Lys	Pro	Ser	His	His	Phe	Lys	Glu	Lys	145	150	155
His	Pro	His	Leu	Cys	Ala	Val	Val	Asn	Asp	Glu	Ser	Asp	Pro	Leu	Lys	165	170	175
Arg	Gly	Phe	Ala	Ser	Phe	Val	Ala	Ser	Asn	Pro	Asn	Ala	Pro	Lys	Arg	180	185	190
Asn	Ala	Phe	Tyr	Asp	Ala	Leu	Asn	Ser	Ile	Glu	Pro	Val	Thr	Gly	Gly	195	200	205
Gly	Ser	Val	Lys	Asn	Thr	Leu	Gly	Tyr	Lys	Val	Gly	Asn	Lys	Asn	Glu	210	215	220
Phe	Leu	Ser	Gln	Tyr	Lys	Phe	Asn	Leu	Cys	Phe	Glu	Asn	Ser	Gln	Gly	225	230	235
Tyr	Gly	Tyr	Val	Thr	Glu	Lys	Ile	Ile	Asp	Ala	Tyr	Phe	Ser	His	Thr	245	250	255
Ile	Pro	Ile	Tyr	Trp	Gly	Ser	Pro	Ser	Val	Ala	Lys	Asp	Phe	Asn	Pro	260	265	270
Lys	Ser	Phe	Val	Asn	Val	His	Asp	Phe	Lys	Asn	Phe	Asp	Glu	Ala	Ile	275	280	285
Asp	Tyr	Val	Arg	Tyr	Leu	His	Thr	His	Pro	Asn	Ala	Tyr	Leu	Asp	Met	290	295	300
Leu	Tyr	Glu	Asn	Pro	Leu	Asn	Thr	Leu	Asp	Gly	Lys	Ala	Tyr	Phe	Tyr	305	310	315
Gln	Asp	Leu	Ser	Phe	Lys	Lys	Ile	Leu	Asp	Phe	Phe	Lys	Thr	Ile	Leu	325	330	335
Glu	Asn	Asp	Thr	Ile	Tyr	His	Asn	Asn	Pro	Phe	Val	Phe	Tyr	Arg	Asp	340	345	350
Leu	Asn	Glu	Pro	Leu	Val	Ser	Ile	Asp	Asp	Leu	Arg	Ala	Asp	Tyr	Asn	355	360	365

Asn Leu Arg Ala Asp Tyr Asn Asn Leu Arg Ala Asp Tyr Asn Asn Leu
 370 375 380
 Arg Ala Asp Tyr Asn Asn Leu Arg Ala Asp Tyr Asp Arg Leu Leu Gln
 385 390 395 400
 Asn Arg Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys Ile
 405 410 415
 Tyr His Lys Ala Tyr His Lys Ser Leu Pro Leu Leu Arg Ala Ile Arg
 420 425 430
 Arg Trp Val Lys Lys Leu Gly Leu
 435 440

<210> 19
 <211> 1664
 <212> DNA
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 948 FutA fucosyltransferase

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 gtatttcaaa cgccatttga gtttgccata attggtttaa aggataaaaa tggtccagcc 180
 ctactagac gctttcatag acagcaccga tttagatgaa acaaccata agccccatt 240
 aaatgtagcc ctagccaatt ggtggccctt aaaaaatagc gaaaaaaaaag gattcagaga 300
 cttcattttg catttcattcc taaaacaacg ctataaaaatc attctgcaca gcaaccctaa 360
 tgaaccctca gatctagtct ttggcaatcc tttggaacaa gccagaaaaa tcttatctta 420
 tcaaaacact aaacgagtggt tttacaccgg cgaaaatgaa gtgcctaatt tcaatctctt 480
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 cttgagggca tgctcgcccc ttcagccacg catttgcacc cattagaaaag gaggggtttg 1620
 cggaattcct gcagcccggg ggatcccccg ggctgcagga attc 1664

<210> 20
 <211> 456
 <212> PRT
 <213> Helicobacter pylori

<220>

<223> H. pylori strain 948 FutA fucosyltransferase

<400> 20

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Glu Thr Thr His Lys Pro Pro Leu Asn Val Ala Leu Ala Asn Trp Trp
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Pro Leu Lys Asn Ser Glu Lys Lys Gly Phe Arg Asp Phe Ile Leu His
35 40 45
Phe Ile Leu Lys Gln Arg Tyr Lys Ile Ile Leu His Ser Asn Pro Asn
50 55 60
Glu Pro Ser Asp Leu Val Phe Gly Asn Pro Leu Glu Gln Ala Arg Lys
65 70 75 80
Ile Leu Ser Tyr Gln Asn Thr Lys Arg Val Phe Tyr Thr Gly Glu Asn
85 90 95
Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
100 105 110
Leu Asp Phe Asn Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala Tyr
115 120 125
Leu His Tyr Lys Ala Met Leu Val Asn Asp Thr Thr Ser Pro Tyr Lys
130 135 140
Leu Lys Ala Leu Tyr Thr Leu Lys Lys Pro Ser His Lys Phe Lys Glu
145 150 155 160
Asn His Pro Asn Leu Cys Ala Leu Ile His Asn Glu Ser Asp Pro Trp
165 170 175
Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro Ile
180 185 190
Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ala Ile Glu Pro Val Ala Ser
195 200 205
Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Lys Val Lys Asn Lys Asn
210 215 220
Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Ser Gln
225 230 235 240
Gly Tyr Gly Tyr Val Thr Glu Lys Ile Leu Asp Ala Tyr Phe Ser His
245 250 255
Thr Ile Pro Ile Tyr Trp Gly Ser Pro Ser Val Ala Lys Asp Phe Asn
260 265 270
Pro Lys Ser Phe Val Asn Val His Asp Phe Asn Asn Phe Asp Glu Ala
275 280 285
Ile Asp Tyr Ile Arg Tyr Leu His Ala His Gln Asn Ala Tyr Leu Asp
290 295 300

Met Leu Tyr Glu Asn Pro Leu Asn Thr Ile Asp Gly Lys Ala Gly Phe
305 310 315 320

Tyr Gln Asp Leu Ser Phe Glu Lys Ile Leu Asp Phe Phe Lys Asn Ile
325 330 335

Leu Glu Asn Asp Thr Ile Tyr His Cys Asn Asp Ala His Tyr Ser Ala
340 345 350

Leu His Arg Asp Leu Asn Glu Pro Leu Val Ser Val Asp Asp Leu Arg
355 360 365

Arg Asp His Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn
370 375 380

Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp
385 390 395 400

Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Arg Asp His Asp Asp Leu
405 410 415

Arg Arg Asp His Glu Arg Leu Leu Ser Lys Ala Thr Pro Leu Leu Glu
420 425 430

Leu Ser Gln Asn Thr Ser Phe Lys Ile Tyr Arg Lys Ala Tyr Gln Lys
435 440 445

Ser Leu Pro Leu Leu Arg Ala Ile
450 455

<210> 21
<211> 1895
<212> DNA
<213> Helicobacter pylori

<220>
<223> H. pylori strain 955 FutA fucosyltransferase

<400> 21
ggatcccagag cgaccaatca ttacagggat ttattaaatt tagatgtggc tttcagtaac 60
acgctgatag tggaaaatgg tgccttaaac ggcttggtta cggggcatat gatgttttca 120
cactctaaag gcgaaatgct tctcgcccta caacgcttgc taaatatcag tgaaacgagc 180
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ggataaagat gttccagccc ctattagatg ccttcataga aagcgcttca attaaaaaaa 420
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aaagaatttta aagcgagcgt tctttatttc atcctaaaac aacgctataa aatcattctg 540
cacagcaacc ctaatgaacc ctcagatcta gtcttttgga atcctttgga acaagccaga 600
aaaatcttat cttatcaaaa cactaaacga gtgttttaca ccggcgaaaa tgaagtgcct 660
aatttcaatc tctttgatta cgccataggc tttgatgaat tggattttta cgatcgctat 720
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tattttattgg gggagtccca gcgtggcgaa agatttttaac cctaaaagtt ttgtgaatgt 1200
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aaacgcttat ttagacatgc tttatgaaaa ccccttaaacc accattgatg ggaaagcggg 1320
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cgatacgatt tatcattgca atgatgccca ttattctgct cttcatcgtg atttgaatga 1440
gccgtagtg tctgttgatg atttgagaag agatcatgat gatttgaggg ttaattatga 1500
tgatttgaga agagatcatg aacgcctctt atcaaaggct acccctcttt tggagctatc 1560
ccaaaacacc tcttttaaaa tctatcgcaa agcttatcaa aagtccttac cttgttgcg 1620
tgccataagg aagtgggtta aaaaataagg cgtattttta gactgatgaa gaaattgaag 1680
cgctatttta aaatgcgcta acgcttcttt tttgagcgtg gggtttttga gcatgtcctc 1740
taaagcatgg gtgcttaaaa aatgttttgt ttttaaagac acgatgcgtc caaaggattc 1800
ttcttttagaa aggttttaaaa ggcgtttggg caaaatctcg ccaaatacca caatgacttt 1860
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```

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<210> 22
<211> 49
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:H. pylori
      strain 955 FutA fucosyltransferase coding
      sequence amino acid translation peptide

```

```

<400> 22
Met Phe Lys His Ala His Ile Lys Ile Ala Phe Asn Ala Lys Glu Val
  1             5             10             15
Leu Lys Gln His Ala Thr His Cys Ile Asn Glu Pro Asp Leu Ala Leu
      20             25             30
Ile Lys Pro Leu Ile Phe Lys Ile Phe Phe Val Lys Tyr Ser Phe Lys
      35             40             45

```

Gly

```

<210> 23
<211> 6
<212> PRT
<213> Artificial Sequence

```

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<220>
<223> Description of Artificial Sequence:H. pylori
      strain 955 FutA fucosyltransferase coding
      sequence amino acid translation peptide

```

```

<400> 23
Arg Cys Ser Ser Pro Tyr
  1             5

```

```

<210> 24
<211> 10
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:H. pylori
      strain 955 FutA fucosyltransferase coding
      sequence amino acid translation peptide

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<400> 24

Lys Ala Leu Gln Leu Lys Lys Asn Cys Leu
1 5 10

<210> 25

<211> 227

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 25

Ile Ser Pro Pro Leu Lys Ile Ala Val Ala Asn Trp Phe Asn Gly Thr
1 - 5 10 15

Lys Glu Phe Lys Ala Ser Val Leu Tyr Phe Ile Leu Lys Gln Arg Tyr
20 25 30

Lys Ile Ile Leu His Ser Asn Pro Asn Glu Pro Ser Asp Leu Val Phe
35 40 45

Gly Asn Pro Leu Glu Gln Ala Arg Lys Ile Leu Ser Tyr Gln Asn Thr
50 55 60

Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Val Pro Asn Phe Asn Leu
65 70 75 80

Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Phe Asn Asp Arg Tyr
85 90 95

Leu Arg Met Pro Leu Tyr Tyr Ala Tyr Leu His Tyr Lys Ala Met Leu
100 105 110

Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu Lys Ala Leu Tyr Thr Leu
115 120 125

Lys Lys Pro Ser His Lys Phe Lys Glu Asn His Pro Asn Leu Cys Ala
130 135 140

Leu Ile His Asn Glu Ser Asp Pro Trp Lys Arg Gly Phe Ala Ser Phe
145 150 155 160

Val Ala Ser Asn Pro Asn Ala Pro Ile Arg Asn Ala Phe Tyr Asp Ala
165 170 175

Leu Asn Ala Ile Glu Pro Val Ala Ser Gly Gly Ser Val Lys Asn Thr
180 185 190

Leu Gly Tyr Lys Val Lys Asn Lys Asn Glu Phe Leu Ser Gln Tyr Lys
195 200 205

Phe Asn Leu Cys Phe Glu Asn Ser Gln Gly Tyr Gly Tyr Val Thr Glu
210 215 220

Lys Ile Pro
225

<210> 26
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 26
Cys Val Phe Gln Pro His Tyr Pro Tyr Leu Leu Gly Glu Ser Gln Arg
1 5 10 15

Gly Glu Arg Phe
20

<210> 27
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 27
Lys Phe Cys Glu Cys Ala
1 5

<210> 28
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 28
Phe Gln Gln Leu
1

<210> 29
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 29
 Leu Tyr Gln Ile Phe Thr Arg Ala Pro Lys Arg Leu Phe Arg His Ala
 1 5 10 15

Leu

<210> 30
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 30 -
 Lys Pro Leu Lys His His
 1 5

<210> 31
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 31
 Trp Glu Ser Gly Phe Leu Pro Arg Phe Glu Phe
 1 5 10

<210> 32
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 32
 Lys Asp Leu Arg Phe Phe Gln Lys His Ser
 1 5 10

<210> 33
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 33
Lys Arg Tyr Asp Leu Ser Leu Gln
1 5

<210> 34
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 34
Cys Pro Leu Phe Cys Ser Ser Ser
1 5

<210> 35
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 35
Ala Val Ser Val Cys
1 5

<210> 36
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 36
Phe Glu Lys Arg Ser
1 5

<210> 37
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 37

Thr Pro Leu Ile Lys Gly Tyr Pro Ser Phe Gly Ala Ile Pro Lys His
1 5 10 15

Leu Phe

<210> 38

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 38 -

Asn Leu Ser Gln Ser Leu Ser Lys Val Leu Thr Leu Val Ala Cys His
1 5 10 15

Lys Glu Val Gly
20

<210> 39

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 39

Lys Ile Arg Arg Ile Leu Arg Leu Met Lys Lys Leu Lys Arg Tyr Phe
1 5 10 15

Lys Met Arg

<210> 40

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:H. pylori
strain 955 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 40

Arg Phe Phe Phe Glu Arg Gly Val Phe Glu His Val Leu
1 5 10

<210> 41

<211> 4

<212> PRT

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

 <400> 41
 Ser Met Gly Ala
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 <210> 42
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

 <400> 42
 Lys Met Phe Cys Phe
 1 5

 <210> 43
 <211> 13
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

 <400> 43
 Arg His Asp Ala Ser Lys Gly Phe Phe Phe Arg Lys Val
 1 5 10

 <210> 44
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

 <400> 44
 Lys Ala Phe Gly Gln Asn Leu Ala Lys Tyr His Asn Asp Phe
 1 5 10

 <210> 45
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 45
 Ser Ala Val Val
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<210> 46
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 955 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 46
 Leu Pro Gly Arg Asn
 1 5

<210> 47
 <211> 1742
 <212> DNA
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 1218 FutA fucosyltransferase

<400> 47
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 tacctttttg gtagcgatac ctttcgctct cgtgatcttg gcttatttca aacgccattt 120
 gagtttgcct aaattgggtt aaaggataac catgttccaa cccctattag acgcttatat 180
 agaaaagcgt tccattgaaa aaattacctc taaatctccc cccccctaa aaatcgctgt 240
 ggcgaattgg tggggagatg aagagggtga agaatttaaa aagaacattc tttattttat 300
 tctcagtcag cattacacaa tcacctcca ccaaaacccc aacgaaccct ccgatctcgt 360
 ctttggcagt cctattggat cagccagaaa aatcttatcc tatcaaaacg caaaaagagt 420
 gttttacacc ggtgaaaacg aatcgccata tttcaacctc tttgattacg ccataggctt 480
 tgatgaatgg attttagaga tcgttattta agaatgcctt tatattatga tagactacac 540
 cataaagccg agagcgtgaa tgacaccact tcgccttaca aactcaaacc tgacagcctt 600
 tatgctttta aaaaaccctc ccatcatttt aaagaaaacc accccaattt atgcgcagta 660
 gtgaacaatg agagcgatcc tttgaaaaga ggggttgcga gttttgtagc gagcaaccct 720
 aacgctccta aaaggaatgc tttctatgac gcttttaaatt ctatagagcc agttattggg 780
 ggagggagcg tgaaaaacac tttaggctat aacattaaaa acaagagcga gtttttaagc 840
 caatacaaat tcaatctgtg ttttgaaaac tcacaaggct atggctatgt aactgaaaaa 900
 atcattgacg cttacttttag ccataccatt cctatttatt gggggagtcc tagcgtggca 960
 caagatttta accctaagag ttttgtgaat gtttgtgatt ttaaagattt tgatgaagcg 1020
 attgatcatg tgcgatactt gcacacgcac ccaaacgctt atttagacat gctttatgaa 1080
 aaccctttta acacccttga tgggaaagct tactttccaa aatttgagtt taaaaaaat 1140
 cctagatttt tttaaaacga tccttagaaaa cgacacgatt tatcacgata acccttttat 1200
 tttttatcgt gatttgaatg agccgttaat atctattgat gatttgaggg ttaattatga 1260
 tgatttgagg gttaattatg atgatttgag ggtaattat gatgatttga gggtaatta 1320
 tgatgatttg aggggttaatt atgatgattt gagggttaat tatgatgatt tgaggggtta 1380
 ttatgatgat ttgagggtta attatgatga tttgagggtt aattgtgatg atttgaggg 1440
 taattatgat gatttgaggg ttaattatga gcggctctta caaaacgcct cgcctttatt 1500
 agaactctct caaaacacca cttttaaaat ctatcgcaaa gcttatcaaa aatccttacc 1560
 tttgttgcgt gcggcgagaa agttgattaa aaaattgggt ttgtaaaatt gggggtaata 1620

aaaccccttg cgctatcatc gcagacgcca cttttctaaa accagcgata ttagccccta 1680
aaacaaaatt agtaggggtct ttaaactctt tagcggtttg agagacattc ttataagaat 1740
tc 1742

<210> 48
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 1218 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 48
Met Phe Gln Pro Leu Leu Asp Ala Tyr Ile Glu Ser Ala Ser Ile Glu
1 - 5 10 15
Lys Ile Thr Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala Asn
20 25 30
Trp Trp Gly Asp Glu Glu Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr
35 40 45
Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn
50 55 60
Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys
65 70 75 80
Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn
85 90 95
Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
100 105 110
Trp Ile Leu Glu Ile Val Ile
115

<210> 49
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H. pylori
strain 1218 FutA fucosyltransferase coding
sequence amino acid translation peptide

<400> 49
Glu Cys Leu Tyr Ile Met Ile Asp Tyr Thr Ile Lys Pro Arg Ala
1 5 10 15

<210> 50
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 50
 Met Thr Pro Leu Arg Leu Thr Asn Ser Asn Leu Thr Ala Phe Met Leu
 1 5 10 15

<210> 51
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 51
 Lys Asn Pro Pro Ile Ile Leu Lys Lys Thr Thr Pro Ile Tyr Ala Gln
 1 5 10 15

<210> 52
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 52
 Thr Met Arg Ala Ile Leu
 1 5

<210> 53
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 53
 Lys Glu Gly Leu Arg Val Leu
 1 5

<210> 54
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 54
 Arg Ala Thr Leu Thr Leu Leu Lys Gly Met Leu Ser Met Thr Leu
 1 5 10 15

<210> 55
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 55
 Ser Gln Leu Leu Gly Glu Gly Ala
 1 5

<210> 56
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 56
 Ala Ile Thr Leu Lys Thr Arg Ala Ser Phe
 1 5 10

<210> 57
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 57
 Ala Asn Thr Asn Ser Ile Cys Val Leu Lys Thr His Lys Ala Met Ala
 1 5 10 15

Met

<210> 58
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 58
 Leu Lys Lys Ser Leu Thr Leu Thr Leu Ala Ile Pro Phe Leu Phe Ile
 1 5 10 15
 Gly Gly Val Leu Ala Trp His Lys Ile Leu Thr Leu Arg Val Leu
 20 25 30

<210> 59
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 59
 Met Phe Val Ile Leu Lys Ile Leu Met Lys Arg Leu Ile Met Cys Asp
 1 5 10 15
 Thr Cys Thr Arg Thr Gln Thr Leu Ile
 20 25

<210> 60
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 60
 Thr Cys Phe Met Lys Thr Leu
 1 5

<210> 61
 <211> 171
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:H. pylori
 strain 1218 FutA fucosyltransferase coding
 sequence amino acid translation peptide

<400> 61
 Thr Pro Leu Met Gly Lys Leu Thr Phe Gln Asn Leu Ser Phe Lys Lys
 1 5 10 15

```

Ile Leu Asp Phe Phe Lys Thr Ile Leu Glu Asn Asp Thr Ile Tyr His
      20              25              30
Asp Asn Pro Phe Ile Phe Tyr Arg Asp Leu Asn Glu Pro Leu Ile Ser
      35              40              45
Ile Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp
      50              55              60
Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu
      65              70              75              80
Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val
      85              90              95
Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Cys
      100             105             110
Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg
      115             120             125
Leu Leu Gln Asn Ala Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr
      130             135             140
Phe Lys Ile Tyr Arg Lys Ala Tyr Gln Lys Ser Leu Pro Leu Leu Arg
      145             150             155             160
Ala Ala Arg Lys Leu Ile Lys Lys Leu Gly Leu
      165             170

```

```

<210> 62
<211> 20
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:H. pylori
      strain 1218 FutA fucosyltransferase coding
      sequence amino acid translation peptide

```

```

<400> 62
Ser Asn Pro Leu Arg Tyr His Arg Arg Arg His Leu Ser Lys Thr Ser
  1              5              10              15

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```

Asp Ile Ser Pro
      20

```

```

<210> 63
<211> 35
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:H. pylori
      strain 1218 FutA fucosyltransferase coding
      sequence amino acid translation peptide

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<400> 63

Asn Lys Ile Ser Arg Val Phe Lys Leu Phe Ser Gly Leu Arg Asp Ile
1 5 10 15

Leu Ile Arg Ile Arg Tyr Gln Ala Tyr Arg Tyr Arg Arg Pro Arg Gly
20 25 30

Gly Ala Arg
35

<210> 64

<211> 231

<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1182 FutB fucosyltransferase
catalytic domain conserved region positions 23-305

<400> 64

Pro Pro Pro Leu Lys Ile Ala Val Ala Asn Trp Trp Gly Asp Glu Glu
1 5 10 15

Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr Phe Ile Leu Ser Gln His
20 25 30

Tyr Thr Ile Thr Leu His Gln Asn Pro Asn Glu Pro Ser Asp Leu Val
35 40 45

Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys Ile Leu Ser Tyr Gln Asn
50 55 60

Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Ser Pro Asn Phe Asn
65 70 75 80

Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Phe Arg Asp Arg
85 90 95

Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg Leu His His Lys Ala Glu
100 105 110

Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu Lys Pro Asp Ser Leu
115 120 125

Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys Glu Asn His Pro Asn
130 135 140

Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro Leu Lys Arg Gly Phe
145 150 155 160

Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro Lys Arg Asn Ala Phe
165 170 175

Tyr Asp Val Leu Asn Ser Ile Glu Pro Val Ile Gly Gly Gly Ser Val
180 185 190

Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn Lys Ser Glu Phe Leu Ser
195 200 205

Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Ser Gln Gly Tyr Gly Tyr
 210 215 220

Val Thr Glu Lys Ile Ile Asp
 225 230

<210> 65
 <211> 291
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:glycosyltransferase family 10
 fucosyltransferase consensus sequence pfam00852
 positions 11-301

<400> 65
 Thr Val Pro Leu Leu Leu Ala Ile Tyr Thr Trp Trp Ser Leu Ile Glu
 1 5 10 15
 Tyr Lys Glu Trp Lys Lys Ser Pro Ile Tyr Phe Ile Gly Ser Gln Ala
 20 25 30
 Pro Gln Pro Pro Leu Arg Ile Leu Leu Trp Thr Trp Pro Phe Asn Gly
 35 40 45
 Asn Pro Leu Ala Leu Ser Asp Cys Pro Leu Ser Tyr Gln Asn Thr Ala
 50 55 60
 Arg Cys Arg Leu Thr Ala Asn Arg Ser Pro Leu Glu Ser Ala Asp Ala
 65 70 75 80
 Val Leu Phe His His Arg Asp Leu Ser Lys Gly Phe Pro Asp Leu Pro
 85 90 95
 Pro Ser Pro Arg Pro Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu
 100 105 110
 Ser Pro Ser Asn Ser Gly Leu Asn Asp Leu Arg Asp Gly Tyr Phe Asn
 115 120 125
 Trp Thr Leu Ser Tyr Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly
 130 135 140
 Tyr Leu Glu Pro Arg Leu Ser Gln Val Val Asn Ala Pro Leu Leu Ser
 145 150 155 160
 Ala Lys Arg Lys Gly Ala Ala Trp Val Val Ser Asn Cys Asn Thr Arg
 165 170 175
 Ser Lys Arg Glu Arg Phe Tyr Lys Gln Leu Asn Lys His Leu Gln Val
 180 185 190
 Asp Val Gly Gly Arg Val Ala Asn Pro Leu Pro Leu Lys Val Gly Cys
 195 200 205
 Leu Val Glu Thr Leu Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn
 210 215 220

Ser Gln His Tyr Asp Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu
 225 230 235 240
 Gln Ala Gly Thr Ile Pro Val Val Leu Gly Pro Arg Ala Val Tyr Glu
 245 250 255
 Asp Phe Val Pro Pro Lys Ser Phe Ile His Val Asp Asp Phe Lys Ser
 260 265 270
 Pro Lys Glu Leu Ala Asp Tyr Leu Leu Tyr Leu Asp Thr Asn Pro Thr
 275 280 285
 Ala Tyr Ser
 290

<210> 66
 <211> 391 -
 <212> PRT
 <213> *Helicobacter pylori*

<220>
 <223> *H. pylori* strain 1111 FutA fucosyltransferase
 catalytic domain conserved region positions 27-417

<400> 66
 Ile Ala Val Ala Asn Trp Trp Gly Asp Glu Glu Ile Lys Lys Phe Lys
 1 5 10 15
 Lys Ser Val Leu Tyr Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu
 20 25 30
 His Arg Asn Pro Asp Lys Pro Ala Asp Ile Val Phe Gly Asn Pro Leu
 35 40 45
 Gly Ser Ala Arg Lys Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe
 50 55 60
 Tyr Thr Gly Glu Asn Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala
 65 70 75 80
 Ile Gly Phe Asp Glu Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro
 85 90 95
 Leu Tyr Tyr Ala Tyr Leu His Tyr Lys Ala Glu Leu Val Asn Asp Thr
 100 105 110
 Thr Ser Pro Tyr Lys Leu Gln Pro Asp Ser Leu Tyr Ala Leu Lys Lys
 115 120 125
 Pro Ser His His Phe Lys Glu Asn His Pro Asn Leu Cys Ala Val Val
 130 135 140
 Asn Asn Glu Ser Asp Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala
 145 150 155 160
 Ser Asn Pro Asn Ala Pro Arg Arg Asn Ala Phe Tyr Glu Ala Leu Asn
 165 170 175
 Ala Ile Glu Pro Val Ala Gly Gly Gly Ser Val Lys Asn Thr Leu Gly
 180 185 190

Tyr Asn Val Lys Asn Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn
 195 200 205
 Leu Cys Phe Glu Asn Thr Gln Gly Tyr Gly Tyr Val Thr Glu Lys Ile
 210 215 220
 Ile Asp Ala Tyr Phe Ser His Thr Ile Pro Ile Tyr Trp Gly Ser Pro
 225 230 235 240
 Ser Val Ala Lys Asp Phe Asn Pro Lys Ser Phe Val Asn Val His Asp
 245 250 255
 Phe Asn Asn Phe Asp Glu Ala Ile Asp Tyr Ile Arg Tyr Leu His Thr
 260 265 270
 His Pro Asn Ala Tyr Leu Asp Met His Tyr Glu Asn Pro Leu Asn Thr
 275 280 285
 Ile Asp Gly Lys Ala Tyr Phe Tyr Gln Asn Leu Ser Phe Lys Lys Ile
 290 295 300
 Leu Asp Phe Phe Lys Thr Ile Leu Glu Asn Asp Thr Ile Tyr His Asp
 305 310 315 320
 Asn Pro Phe Ile Phe Tyr Arg Asp Leu Asn Glu Pro Ser Val Ser Ile
 325 330 335
 Asp Gly Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp
 340 345 350
 Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Glu Arg Leu Leu
 355 360 365
 Gln Asn Ala Ser Pro Leu Leu Glu Leu Ser Gln Asn Thr Thr Phe Lys
 370 375 380
 Ile Tyr Arg Lys Ala Tyr Gln
 385 390

<210> 67
 <211> 336
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:glycosyltransferase family 10
 fucosyltransferase consensus sequence pfam00852
 positions 16-351

<400> 67
 Leu Ala Ile Tyr Thr Trp Trp Ser Leu Ile Glu Tyr Lys Glu Trp Lys
 1 5 10 15
 Lys Ser Pro Ile Tyr Phe Ile Gly Ser Gln Ala Pro Gln Pro Pro Leu
 20 25 30
 Arg Ile Leu Leu Trp Thr Trp Pro Phe Asn Gly Asn Pro Leu Ala Leu
 35 40 45

Ser Asp Cys Pro Leu Ser Tyr Gln Asn Thr Ala Arg Cys Arg Leu Thr
 50 55 60
 Ala Asn Arg Ser Pro Leu Glu Ser Ala Asp Ala Val Leu Phe His His
 65 70 75 80
 Arg Asp Leu Ser Lys Gly Phe Pro Asp Leu Pro Pro Ser Pro Arg Pro
 85 90 95
 Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu Ser Pro Ser Asn Ser
 100 105 110
 Gly Leu Asn Asp Leu Arg Asp Gly Tyr Phe Asn Trp Thr Leu Ser Tyr
 115 120 125
 Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly Tyr Leu Glu Pro Arg
 130 135 140
 Leu Ser Gln Val Val Asn Ala Pro Leu Leu Ser Ala Lys Arg Lys Gly
 145 150 155 160
 Ala Ala Trp Val Val Ser Asn Cys Asn Thr Arg Ser Lys Arg Glu Arg
 165 170 175
 Phe Tyr Lys Gln Leu Asn Lys His Leu Gln Val Asp Val Gly Gly Arg
 180 185 190
 Val Ala Asn Pro Leu Pro Leu Lys Val Gly Cys Leu Val Glu Thr Leu
 195 200 205
 Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser Gln His Tyr Asp
 210 215 220
 Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu Gln Ala Gly Thr Ile
 225 230 235 240
 Pro Val Val Leu Gly Pro Arg Ala Val Tyr Glu Asp Phe Val Pro Pro
 245 250 255
 Lys Ser Phe Ile His Val Asp Asp Phe Lys Ser Pro Lys Glu Leu Ala
 260 265 270
 Asp Tyr Leu Leu Tyr Leu Asp Thr Asn Pro Thr Ala Tyr Ser Glu Tyr
 275 280 285
 Phe Glu Trp Arg Tyr Asp Leu Arg Val Arg Leu Phe Ser Trp Asp Ala
 290 295 300
 Leu Arg Tyr Asp Glu Gly Phe Cys Arg Val Cys Arg Leu Leu Gln Asn
 305 310 315 320
 Ala Pro Asp Arg Tyr Lys Thr Tyr Pro Asn Ile Ala Lys Trp Phe Gln
 325 330 335

<210> 68

<211> 377

<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1218 FutB fucosyltransferase
catalytic domain conserved region positions 23-399

<400> 68

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Pro Pro Pro Leu Lys Ile Ala Val Ala Asn Trp Trp Gly Asp Glu Glu
  1           5           10           15

Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr Phe Ile Leu Ser Gln His
  20           25           30

Tyr Thr Ile Thr Leu His Gln Asn Pro Asn Glu Pro Ser Asp Leu Val
  35           40           45

Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys Ile Leu Ser Tyr Gln Asn
  50           55           60

Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Ser Pro Asn Phe Asn
  65           70           75           80

Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Phe Arg Asp Arg
  85           90           95

Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg Leu His His Lys Ala Glu
 100          105          110

Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu Lys Pro Asp Ser Leu
 115          120          125

Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys Glu Asn His Pro Asn
 130          135          140

Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro Leu Lys Arg Gly Phe
 145          150          155          160

Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro Lys Arg Asn Ala Phe
 165          170          175

Tyr Asp Ala Leu Asn Ser Ile Glu Pro Val Ile Gly Gly Gly Ser Val
 180          185          190

Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn Lys Ser Glu Phe Leu Ser
 195          200          205

Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Ser Gln Gly Tyr Gly Tyr
 210          215          220

Val Thr Glu Lys Ile Ile Asp Ala Tyr Phe Ser His Thr Ile Pro Ile
 225          230          235          240

Tyr Trp Gly Ser Pro Ser Val Ala Gln Asp Phe Asn Pro Lys Ser Phe
 245          250          255

Val Asn Val Cys Asp Phe Lys Asp Phe Asp Glu Ala Ile Asp His Val
 260          265          270

Arg Tyr Leu His Thr His Pro Asn Ala Tyr Leu Asp Met Leu Tyr Glu
 275          280          285

Asn Pro Leu Asn Thr Leu Asp Gly Lys Ala Tyr Phe Tyr Gln Asn Leu
 290          295          300
```

Ser Phe Lys Lys Ile Leu Asp Phe Phe Lys Thr Ile Leu Glu Asn Asp
305 310 315 320

Thr Ile Tyr His Asp Asn Pro Phe Ile Phe Tyr Arg Asp Leu Asn Glu
325 330 335

Pro Leu Ile Ser Ile Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg
340 345 350

Val Asn Tyr Asp Asp Leu Arg Val Asn Tyr Asp Asp Leu Arg Val Asn
355 360 365

Tyr Asp Asp Leu Arg Val Asn Tyr Asp
370 375

<210> 69

<211> 341-

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial

Sequence:glycosyltransferase family 10

fucosyltransferase consensus sequence pfam00852

positions 11-351

<400> 69

Thr Val Pro Leu Leu Leu Ala Ile Tyr Thr Trp Trp Ser Leu Ile Glu
1 5 10 15

Tyr Lys Glu Trp Lys Lys Ser Pro Ile Tyr Phe Ile Gly Ser Gln Ala
20 25 30

Pro Gln Pro Pro Leu Arg Ile Leu Leu Trp Thr Trp Pro Phe Asn Gly
35 40 45

Asn Pro Leu Ala Leu Ser Asp Cys Pro Leu Ser Tyr Gln Asn Thr Ala
50 55 60

Arg Cys Arg Leu Thr Ala Asn Arg Ser Pro Leu Glu Ser Ala Asp Ala
65 70 75 80

Val Leu Phe His His Arg Asp Leu Ser Lys Gly Phe Pro Asp Leu Pro
85 90 95

Pro Ser Pro Arg Pro Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu
100 105 110

Ser Pro Ser Asn Ser Gly Leu Asn Asp Leu Arg Asp Gly Tyr Phe Asn
115 120 125

Trp Thr Leu Ser Tyr Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly
130 135 140

Tyr Leu Glu Pro Arg Leu Ser Gln Val Val Asn Ala Pro Leu Leu Ser
145 150 155 160

Ala Lys Arg Lys Gly Ala Ala Trp Val Val Ser Asn Cys Asn Thr Arg
165 170 175

Ser Lys Arg Glu Arg Phe Tyr Lys Gln Leu Asn Lys His Leu Gln Val
 180 185 190
 Asp Val Gly Gly Arg Val Ala Asn Pro Leu Pro Leu Lys Val Gly Cys
 195 200 205
 Leu Val Glu Thr Leu Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn
 210 215 220
 Ser Gln His Tyr Asp Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu
 225 230 235 240
 Gln Ala Gly Thr Ile Pro Val Val Leu Gly Pro Arg Ala Val Tyr Glu
 245 250 255
 Asp Phe Val Pro Pro Lys Ser Phe Ile His Val Asp Asp Phe Lys Ser
 260 265 270
 Pro Lys Glu Leu Ala Asp Tyr Leu Leu Tyr Leu Asp Thr Asn Pro Thr
 275 280 285
 Ala Tyr Ser Glu Tyr Phe Glu Trp Arg Tyr Asp Leu Arg Val Arg Leu
 290 295 300
 Phe Ser Trp Asp Ala Leu Arg Tyr Asp Glu Gly Phe Cys Arg Val Cys
 305 310 315 320
 Arg Leu Leu Gln Asn Ala Pro Asp Arg Tyr Lys Thr Tyr Pro Asn Ile
 325 330 335
 Ala Lys Trp Phe Gln
 340

<210> 70
 <211> 256
 <212> PRT
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 19C2 FutB fucosyltransferase
 catalytic domain conserved region positions 22-277

<400> 70
 Pro Pro Leu Asn Ile Ala Leu Ala Asn Trp Trp Pro Leu Asp Lys Arg
 1 5 10 15
 Glu Ser Lys Gly Phe Arg Lys Lys Phe Ile Leu His Phe Ile Leu Ser
 20 25 30
 Gln His Tyr Thr Ile Ala Leu His Arg Asn Pro Asp Lys Pro Ala Asp
 35 40 45
 Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg Lys Ile Leu Ser Tyr
 50 55 60
 Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu Val Pro Asn
 65 70 75 80
 Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu Asp Phe Arg
 85 90 95

Asp	Arg	Tyr	Leu	Arg	Met	Pro	Leu	Tyr	Tyr	Asp	Arg	Leu	His	His	Lys
			100					105					110		
Ala	Glu	Ser	Val	Asn	Asp	Thr	Thr	Ala	Pro	Tyr	Lys	Ile	Lys	Ser	Asp
		115					120					125			
Ser	Leu	Tyr	Ala	Leu	Lys	Lys	Pro	Ser	His	His	Phe	Lys	Glu	Asn	His
	130					135					140				
Pro	His	Leu	Cys	Ala	Leu	Ile	Asn	Asn	Glu	Ile	Asp	Pro	Leu	Lys	Arg
145					150					155					160
Gly	Phe	Ala	Ser	Phe	Val	Ala	Ser	Asn	Pro	Asn	Ala	Pro	Ile	Arg	Asn
				165					170					175	
Ala	Phe	Tyr	Glu	Ala	Leu	Asn	Ser	Ile	Glu	Pro	Val	Thr	Gly	Gly	Gly
			180					185					190		
Ser	Val	Arg	Asn	Thr	Leu	Gly	Tyr	Asn	Val	Lys	Asn	Lys	Asn	Glu	Phe
		195					200				205				
Leu	Ser	Gln	Tyr	Lys	Phe	Asn	Leu	Cys	Phe	Glu	Asn	Thr	Gln	Gly	Tyr
	210					215					220				
Gly	Tyr	Val	Thr	Glu	Lys	Ile	Ile	Asp	Ala	Tyr	Phe	Ser	His	Thr	Ile
225					230					235					240
Pro	Ile	Tyr	Trp	Gly	Gly	Val	Pro	Ser	Val	Ala	Lys	Asp	Phe	Asn	Pro
				245					250					255	

<210> 71
 <211> 259
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:glycosyltransferase family 10
 fucosyltransferase consensus sequence pfam00852
 positions 12-270

<400> 71															
Val	Pro	Leu	Leu	Leu	Ala	Ile	Tyr	Thr	Trp	Trp	Ser	Leu	Ile	Glu	Tyr
1				5					10					15	
Lys	Glu	Trp	Lys	Lys	Ser	Pro	Ile	Tyr	Phe	Ile	Gly	Ser	Gln	Ala	Pro
			20					25					30		
Gln	Pro	Pro	Leu	Arg	Ile	Leu	Leu	Trp	Thr	Trp	Pro	Phe	Asn	Gly	Asn
		35					40					45			
Pro	Leu	Ala	Leu	Ser	Asp	Cys	Pro	Leu	Ser	Tyr	Gln	Asn	Thr	Ala	Arg
	50					55					60				
Cys	Arg	Leu	Thr	Ala	Asn	Arg	Ser	Pro	Leu	Glu	Ser	Ala	Asp	Ala	Val
65					70					75					80
Leu	Phe	His	His	Arg	Asp	Leu	Ser	Lys	Gly	Phe	Pro	Asp	Leu	Pro	Pro
				85					90					95	

Ser Pro Arg Pro Pro Gly Gln Pro Trp Val Trp Ala Ser Met Glu Ser
 100 105 110
 Pro Ser Asn Ser Gly Leu Asn Asp Leu Arg Asp Gly Tyr Phe Asn Trp
 115 120 125
 Thr Leu Ser Tyr Arg Ala Asp Ser Asp Ala Phe His Pro Tyr Gly Tyr
 130 135 140
 Leu Glu Pro Arg Leu Ser Gln Val Val Asn Ala Pro Leu Leu Ser Ala
 145 150 155 160
 Lys Arg Lys Gly Ala Ala Trp Val Val Ser Asn Cys Asn Thr Arg Ser
 165 170 175
 Lys Arg Glu Arg Phe Tyr Lys Gln Leu Asn Lys His Leu Gln Val Asp
 180 185 190
 Val Gly Gly Arg Val Ala Asn Pro Leu Pro Leu Lys Val Gly Cys Leu
 195 200 205
 Val Glu Thr Leu Ser Gln Tyr Lys Phe Tyr Leu Ala Phe Glu Asn Ser
 210 215 220
 Gln His Tyr Asp Tyr Val Thr Glu Lys Leu Trp Lys Asn Ala Leu Gln
 225 230 235 240
 Ala Gly Thr Ile Pro Val Val Leu Gly Pro Arg Ala Val Tyr Glu Asp
 245 250 255
 Phe Val Pro

<210> 72
 <211> 245
 <212> PRT
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 1111 FutA fucosyltransferase
 positions 1-245 (1111FutA.pep)

<400> 72
 Met Phe Gln Pro Leu Leu Asp Ala Phe Ile Glu Ser Ala Pro Leu Lys
 1 5 10 15
 Lys Trp Pro Leu Asn Leu Pro Pro Leu Lys Ile Ala Val Ala Asn Trp
 20 25 30
 Trp Gly Asp Glu Glu Ile Lys Lys Phe Lys Lys Ser Val Leu Tyr Phe
 35 40 45
 Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Arg Asn Pro Asp Lys
 50 55 60
 Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg Lys Ile
 65 70 75 80
 Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn Glu
 85 90 95

Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu Leu
 100 105 110
 Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala Tyr Leu
 115 120 125
 His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ser Pro Tyr Lys Leu
 130 135 140
 Gln Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe Lys
 145 150 155 160
 Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp Pro
 165 170 175
 Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala Pro
 180 185 190
 Arg Arg Asn Ala Phe Tyr Glu Ala Leu Asn Ala Ile Glu Pro Val Ala
 195 200 205
 Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Val Lys Asn Lys
 210 215 220
 Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn Thr
 225 230 235 240
 Gln Gly Tyr Gly Tyr
 245

<210> 73

<211> 247

<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 26695 FutA fucosyltransferase
 positions 1-247 (26695A.pep)

<400> 73

Met Phe Gln Pro Leu Leu Asp Ala Phe Ile Glu Ser Ala Ser Ile Glu
 1 5 10 15
 Lys Met Ala Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala
 20 25 30
 Asn Trp Trp Gly Asp Glu Glu Ile Lys Glu Phe Lys Lys Ser Val Leu
 35 40 45
 Tyr Phe Ile Leu Ser Gln Arg Tyr Ala Ile Thr Leu His Gln Asn Pro
 50 55 60
 Asn Glu Phe Ser Asp Leu Val Phe Ser Asn Pro Leu Gly Ala Ala Arg
 65 70 75 80
 Lys Ile Leu Ser Tyr Gln Asn Thr Lys Arg Val Phe Tyr Thr Gly Glu
 85 90 95
 Asn Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp
 100 105 110

Glu Leu Asp Phe Asn Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Ala
 115 120 125
 His Leu His Tyr Lys Ala Glu Leu Val Asn Asp Thr Thr Ala Pro Tyr
 130 135 140
 Lys Leu Lys Asp Asn Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His
 145 150 155 160
 Phe Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asp Glu Ser
 165 170 175
 Asp Leu Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Ala Asn
 180 185 190
 Ala Pro Met Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro
 195 200 205
 Val Thr Gly Gly Gly Ser Val Arg Asn Thr Leu Gly Tyr Lys Val Gly
 210 215 220
 Asn Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu
 225 230 235 240
 Asn Ser Gln Gly Tyr Gly Tyr
 245

<210> 74

<211> 246

<212> PRT

<213> Helicobacter pylori

<220>

<223> H. pylori strain 1182 FutB fucosyltransferase
 positions 1-246 (1182B.pep)

<400> 74

Met Phe Gln Pro Leu Leu Asp Ala Tyr Ile Glu Ser Ala Ser Ile Glu
 1 5 10 15
 Lys Ile Thr Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala Asn
 20 25 30
 Trp Trp Gly Asp Glu Glu Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr
 35 40 45
 Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn
 50 55 60
 Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys
 65 70 75 80
 Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn
 85 90 95
 Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
 100 105 110
 Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg
 115 120 125

Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys
 130 135 140
 Leu Lys Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe
 145 150 155 160
 Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp
 165 170 175
 Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala
 180 185 190
 Pro Lys Arg Asn Ala Phe Tyr Asp Val Leu Asn Ser Ile Glu Pro Val
 195 200 205
 Ile Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn
 210 215 220
 Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn
 225 230 235 240
 Ser Gln Gly Tyr Gly Tyr
 245

<210> 75
 <211> 246
 <212> PRT
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 1218 FutB fucosyltransferase
 positions 1-246 (1218B.pep)

<400> 75
 Met Phe Gln Pro Leu Leu Asp Ala Tyr Ile Glu Ser Ala Ser Ile Glu
 1 5 10 15
 Lys Ile Thr Ser Lys Ser Pro Pro Pro Leu Lys Ile Ala Val Ala Asn
 20 25 30
 Trp Trp Gly Asp Glu Glu Val Glu Glu Phe Lys Lys Asn Ile Leu Tyr
 35 40 45
 Phe Ile Leu Ser Gln His Tyr Thr Ile Thr Leu His Gln Asn Pro Asn
 50 55 60
 Glu Pro Ser Asp Leu Val Phe Gly Ser Pro Ile Gly Ser Ala Arg Lys
 65 70 75 80
 Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu Asn
 85 90 95
 Glu Ser Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp Glu
 100 105 110
 Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp Arg
 115 120 125
 Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ser Pro Tyr Lys
 130 135 140

Leu Lys Pro Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His Phe
 145 150 155 160
 Lys Glu Asn His Pro Asn Leu Cys Ala Val Val Asn Asn Glu Ser Asp
 165 170 175
 Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn Ala
 180 185 190
 Pro Lys Arg Asn Ala Phe Tyr Asp Ala Leu Asn Ser Ile Glu Pro Val
 195 200 205
 Ile Gly Gly Gly Ser Val Lys Asn Thr Leu Gly Tyr Asn Ile Lys Asn
 210 215 220
 Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu Asn
 225 230 235 240
 Ser Gln Gly Tyr Gly Tyr
 245

<210> 76
 <211> 247
 <212> PRT
 <213> *Helicobacter pylori*

<220>
 <223> *H. pylori* strain 19C2 FutB fucosyltransferase
 positions 1-247 (ORF19C2B.pep)

<400> 76
 Met Phe Gln Pro Leu Leu Asp Ala Tyr Ile Asp Ser Thr Arg Leu Asp
 1 5 10 15
 Glu Thr Asp Tyr Lys Pro Pro Leu Asn Ile Ala Leu Ala Asn Trp Trp
 20 25 30
 Pro Leu Asp Lys Arg Glu Ser Lys Gly Phe Arg Lys Lys Phe Ile Leu
 35 40 45
 His Phe Ile Leu Ser Gln His Tyr Thr Ile Ala Leu His Arg Asn Pro
 50 55 60
 Asp Lys Pro Ala Asp Ile Val Phe Gly Asn Pro Leu Gly Ser Ala Arg
 65 70 75 80
 Lys Ile Leu Ser Tyr Gln Asn Ala Lys Arg Val Phe Tyr Thr Gly Glu
 85 90 95
 Asn Glu Val Pro Asn Phe Asn Leu Phe Asp Tyr Ala Ile Gly Phe Asp
 100 105 110
 Glu Leu Asp Phe Arg Asp Arg Tyr Leu Arg Met Pro Leu Tyr Tyr Asp
 115 120 125
 Arg Leu His His Lys Ala Glu Ser Val Asn Asp Thr Thr Ala Pro Tyr
 130 135 140
 Lys Ile Lys Ser Asp Ser Leu Tyr Ala Leu Lys Lys Pro Ser His His
 145 150 155 160

Phe Lys Glu Asn His Pro His Leu Cys Ala Leu Ile Asn Asn Glu Ile
 165 170 175
 Asp Pro Leu Lys Arg Gly Phe Ala Ser Phe Val Ala Ser Asn Pro Asn
 180 185 190
 Ala Pro Ile Arg Asn Ala Phe Tyr Glu Ala Leu Asn Ser Ile Glu Pro
 195 200 205
 Val Thr Gly Gly Gly Ser Val Arg Asn Thr Leu Gly Tyr Asn Val Lys
 210 215 220
 Asn Lys Asn Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu Cys Phe Glu
 225 230 235 240
 Asn Thr Gln Gly Tyr Gly Tyr
 245

<210> 77
 <211> 250
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:fucosyltransferase consensus sequence

<220>
 <221> MOD_RES
 <222> (14)
 <223> Xaa = Pro, Ser or Arg

<220>
 <221> MOD_RES
 <222> (18)
 <223> Xaa = Trp, Met, Ile or Thr

<220>
 <221> MOD_RES
 <222> (19)
 <223> Xaa = Pro, Met, Ala, Thr or Asp

<220>
 <221> MOD_RES
 <222> (22)
 <223> Xaa = Lys, Ser or absent

<220>
 <221> MOD_RES
 <222> (23)
 <223> Xaa = Pro or absent

<220>
 <221> MOD_RES
 <222> (24)
 <223> Xaa = Leu, Ser, Pro or absent

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<220>
<221> MOD_RES
<222> (41)
<223> Xaa = Lys or Glu

<220>
<221> MOD_RES
<222> (42)
<223> Xaa = Lys, Glu or Ser

<220>
<221> MOD_RES
<222> (43)
<223> Xaa = Lys or absent

<220>
<221> MOD_RES
<222> (44)
<223> Xaa = Gly or absent

<220>
<221> MOD_RES
<222> (45)
<223> Xaa = Phe or absent

<220>
<221> MOD_RES
<222> (49)
<223> Xaa = Ser, Asn or Phe

<220>
<221> MOD_RES
<222> (65)
<223> Xaa = Arg or Gln

<220>
<221> MOD_RES
<222> (69)
<223> Xaa = Lys or Glu

<220>
<221> MOD_RES
<222> (102)
<223> Xaa = Val or Ser

<220>
<221> MOD_RES
<222> (131)
<223> Xaa = Ala or Asp

<220>
<221> MOD_RES
<222> (132)
<223> Xaa = Tyr, His or Arg

<220>
<221> MOD_RES
<222> (139)
<223> Xaa = Leu or Ser

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<400> 77															
Met	Phe	Gln	Pro	Leu	Leu	Asp	Ala	Phe	Ile	Glu	Ser	Ala	Xaa	Ile	Glu
1		-		5					10					15	
Lys	Xaa	Xaa	Ser	Lys	Xaa	Xaa	Xaa	Pro	Pro	Leu	Lys	Ile	Ala	Val	Ala
			20					25					30		
Asn	Trp	Trp	Gly	Asp	Glu	Glu	Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Lys	Lys
		35					40					45			
Xaa	Ile	Leu	Tyr	Phe	Ile	Leu	Ser	Gln	His	Tyr	Thr	Ile	Thr	Leu	His
	50					55					60				
Xaa	Asn	Pro	Asx	Xaa	Pro	Ala	Asp	Ile	Val	Phe	Gly	Asn	Pro	Leu	Gly
65					70					75					80
Ser	Ala	Arg	Lys	Ile	Leu	Ser	Tyr	Gln	Asn	Ala	Lys	Arg	Val	Phe	Tyr
				85					90					95	
Thr	Gly	Glu	Asn	Glu	Xaa	Pro	Asn	Phe	Asn	Leu	Phe	Asp	Tyr	Ala	Ile
			100					105					110		
Gly	Phe	Asp	Glu	Leu	Asp	Phe	Arg	Asp	Arg	Tyr	Leu	Arg	Met	Pro	Leu
		115					120					125			
Tyr	Tyr	Xaa	Xaa	Leu	His	His	Lys	Ala	Glu	Xaa	Val	Asn	Asp	Thr	Thr
	130					135					140				
Ser	Pro	Tyr	Lys	Leu	Lys	Xaa	Asp	Ser	Leu	Tyr	Ala	Leu	Lys	Lys	Pro
145				150						155					160
Ser	His	His	Phe	Lys	Glu	Asn	His	Pro	Asn	Leu	Cys	Ala	Val	Val	Asn
				165					170					175	
Asn	Glu	Ser	Asp	Pro	Leu	Lys	Arg	Gly	Phe	Ala	Ser	Phe	Val	Ala	Ser
			180					185					190		
Asn	Pro	Asn	Ala	Pro	Xaa	Arg	Asn	Ala	Phe	Tyr	Asp	Ala	Leu	Asn	Ser
		195					200					205			
Ile	Glu	Pro	Val	Xaa	Gly	Gly	Gly	Ser	Val	Lys	Asn	Thr	Leu	Gly	Tyr
	210					215					220				

Asn Val Lys Asn Lys Ser Glu Phe Leu Ser Gln Tyr Lys Phe Asn Leu
 225 230 235 240

Cys Phe Glu Asn Ser Gln Gly Tyr Gly Tyr
 245 250

<210> 78
 <211> 333
 <212> DNA
 <213> Helicobacter pylori

<220>
 <223> H. pylori strain 915 FutA fucosyltransferase
 (915A.cod(MWG))

<400> 78
 atgttccaac ccctattaga tgcctttata gaaagcgctt ccattgaaaa aatggcctct 60
 aaatctcccc ccctaaaaat cgctgtggcg aattggtggg gagatgaaga aattaaaaaa 120
 tttaaaaaga gcgttcttta ttttatccta agccagcatt acacaatcac ttacaccga 180
 aaccctgata aacctgcgga catcgtcttt ggtaaccccc ttggatcagc cagaaaaatc 240
 ttatcctatc aaaacgcaaa aagggtgttt tacaccggtg aaaatgaagt ccctaacttc 300
 aacctctttg attacgccat aggccttttga tga 333

<210> 79
 <211> 1483
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial
 Sequence:fucosyltransferase consensus sequence

<220>
 <221> modified_base
 <222> (77)..(79)
 <223> n = c or absent

<220>
 <221> modified_base
 <222> (106)..(107)
 <223> n = c or absent

<220>
 <221> modified_base
 <222> (108)..(110)
 <223> n = t or absent

<220>
 <221> modified_base
 <222> (119)
 <223> n = g or absent

<220>
 <221> modified_base
 <222> (152)
 <223> n = t or absent

<220>
<221> modified_base
<222> (153)
<223> n = a or absent

<220>
<221> modified_base
<222> (154)
<223> n = c or absent

<220>
<221> modified_base
<222> (343)
<223> n = t or absent

<220>
<221> modified_base
<222> (809)..(810)
<223> n = g or absent

<220>
<221> modified_base
<222> (816)
<223> n = c or absent

<220>
<221> modified_base
<222> (1063)..(1064)
<223> n = a or absent

<220>
<221> modified_base
<222> (1065)
<223> n = c or absent

<220>
<221> modified_base
<222> (1066)
<223> n = a or absent

<220>
<221> modified_base
<222> (1067)
<223> n = t or absent

<220>
<221> modified_base
<222> (1068)
<223> n = c or absent

<220>
<221> modified_base
<222> (1118)
<223> n = g or absent

<220>
<221> modified_base
<222> (1119)
<223> n = a or absent

<220>
 <221> modified_base
 <222> (1120)
 <223> n = t or absent

<400> 79
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 aaatctcccc ccccmynntt aaaaatcgct gtggcgaatt ggtggnnnnn ggagatgana 120
 gaaattaaag aattttaaaaa garcdttctt tnnnatTTtTa tyctaagyca gcattacaca 180
 atcacycctcc accraaacc yratraacct kcvgaymtcg tctttggyaa yccycttgga 240
 tcagccagaa aaatcttata ctatcaaaac gcaaaaagrg tgttttacac cggtgaaaac 300
 gaakyvccta atttcaacct ctttgattac gccataggct ttngatgaat tggaytttag 360
 agatcgttat ttragaatgc ctttrtatta tgmyhrwytr cacyataaag ccgagmkyyt 420
 kaatgacacc actkcgctt acaaactcaa abctgacagc ctttatgctt taaaaaaacc 480
 ctcccacatcat tttaaagaaa accaccchaa ttrtgcgca gtagtgaaya atgagagcga 540
 tcctttgaaa agagggtttg cgagytttgt mgcragcaac cctaacgctc ctadaaggaa 600
 ygcttttytat gasgctttta attctatwga gccagttayt gggggaggga gcgtgaraaa 660
 cacttttaggc tataabrtya aaaacaarag cgagttttta agccaatata arttcaatct 720
 gtgttttgaa aacwcdcaag gctatggcta tgtaactgaa aaaatcattg acgcttaytt 780
 yagccatacc attcctattt attgggggnn agtccnyagc gtggcrmaag attttaaccc 840
 taaragtttt gtgaatgtby rtgatttyaa mraytttgat gaagcgattg ayyatrtsmr 900
 atacytgcac acgcacccaa acgcttattt agacatgcwy tatgaaaacc ctttaaacac 960
 ymttgatggg aaagcttact tttaccaara tttgagtttt aaaaaaatcc tagatttttt 1020
 taaaacgaty tttagaaaacg ayacgatyta tcacrawwwc ycnnnnnntt tyatktkbka 1080
 kyrygatytg matragcckt yartatcyat tgatgrtnnn ttgagggtta attatgatga 1140
 tttgagggtt aattatgays rkytkwkrsw waaykmtkmk smtttrwkrw wmwytmtsa 1200
 dvryhybwb dbkktmaww awkbbkdkyy kwdrktkmrt kvyrwrrkw krrgggttaa 1320
 wwakkawgat ttgagggtta attatgagcg gctcttacia aacgcctcgc ctttattaga 1380
 actctctcaa aacaccactt ttaaaatcta tcgcaaagct tatcaaaaat ccttaccttt 1440
 gttgcgtgcg gcgagaaagt tgattaaaaa attgggtttg taa 1483

<210> 80
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:"FLAG tag"
 epitope tag recognized by anti-LAG antibody

<400> 80
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 81
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:polyhistidine
 metal chelate affinity purification tag,
 hexahistidine affinity tag

<400> 81
 His His His His His His
 1 5